



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/813,279

Source: OIC

Date Processed by STIC: 8/2/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/813,279

DATE: 08/02/2001  
TIME: 14:49:32

Input Set : A:\sequence listing.txt  
Output Set: N:\CRF3\08022001\I813279.raw

2 <110> APPLICANT: Wood, Keith  
3        Hannah, Rita  
4        Moravec, Richard A.  
6 <120> TITLE OF INVENTION: Method for Detection of ATP  
8 <130> FILE REFERENCE: 10743-6  
10 <140> CURRENT APPLICATION NUMBER: US 09/813,279  
12 <141> CURRENT FILING DATE: 2001-03-19  
14 <150> PRIOR APPLICATION NUMBER: US 60/269,526  
15 <151> PRIOR FILING DATE: 2001-02-16  
17 <160> NUMBER OF SEQ ID NOS: (8) *Sequence 2 missing*  
19 <170> SOFTWARE: Microsoft Word (Text Only Format)

## ERRORED SEQUENCES

21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 544  
23 <212> TYPE: PRT  
24 <213> ORGANISM: Artificial Sequence  
W--> 25 <220> FEATURE: (78-0B10) *do not insert a response to 2207. 2207 is a header only.*  
25  
26 <223> OTHER INFORMATION: Mutant luciferase derived from LucPpe2  
28 <400> SEQUENCE: 1  
29 Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu  
30     1               5                           10                       15  
31 Ala Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr  
32     20              25                           30  
33 Ala Asp Ile Ser Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu  
34     35              40                           45  
35 Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu  
36     50              55                           60  
37 Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys  
38     65              70                           75                       80  
39 Ser Glu Asn Gly Leu Gln Phe Phe Leu Pro Val Ile Ala Ser Leu Tyr  
40     85              90                           95  
41 Leu Gly Ile Ile Ala Ala Pro Val Ser Asp Lys Tyr Ile Glu Arg Glu  
42     100             105                          110  
43 Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Ile Phe Cys Ser  
44     115             120                          125  
45 Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser  
46     130             135                          140  
47 Val Glu Thr Ile Ile Ile Leu Asp Leu Asn Glu Asp Leu Gly Gly Tyr  
48     145             150                          155                       160  
49 Gln Cys Leu Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp  
50     165             170                          175  
51 Val Lys Lys Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala  
52     180             185                          190

Page 1/5

Please consult  
Sequence Rule.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/813,279

DATE: 08/02/2001  
TIME: 14:49:32

Input Set : A:\sequence listing.txt  
Output Set: N:\CRF3\08022001\I813279.raw

53 Leu Val Met Phe Ser Ser Gly Thr Thr Gly Val Pro Lys Gly Val Met  
 54 195 200 205  
 55 Leu Thr His Lys Asn Ile Val Ala Arg Phe Ser Leu Ala Lys Asp Pro  
 56 210 215 220  
 57 Thr Phe Gly Asn Ala Ile Asn Pro Thr Thr Ala Ile Leu Thr Val Ile  
 58 225 230 235 240  
 59 Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr  
 60 245 250 255  
 61 Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe  
 62 260 265 270  
 63 Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Leu Val Pro  
 64 275 280 285  
 65 Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp  
 66 290 295 300  
 67 Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys  
 68 305 310 315 320  
 69 Glu Ile Gly Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg  
 70 325 330 335  
 71 Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro  
 72 340 345 350  
 73 Lys Gly Asp Ala Arg Pro Gly Ser Thr Gly Lys Ile Val Pro Phe His  
 74 355 360 365  
 75 Ala Val Lys Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn  
 76 370 375 380  
 77 Glu Pro Gly Glu Leu Tyr Phe Lys Gly Ala Met Ile Met Lys Gly Tyr  
 78 385 390 395 400  
 79 Tyr Asn Asn Glu Glu Ala Thr Lys Ala Ile Ile Asp Asn Asp Gly Trp  
 80 405 410 415  
 81 Leu Arg Ser Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr  
 82 420 425 430  
 83 Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val  
 84 435 440 445  
 85 Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val  
 86 450 455 460  
 87 Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro  
 E--> 88 465 SEQUENCE LISTING

W--> 89 <110> APPLICANT: Wood, Keith  
 W--> 89 <110> APPLICANT: Wood, Keith  
 W--> 93 <120> TITLE OF INVENTION: Improved Method for Detection of ATP  
 W--> 93 <120> TITLE OF INVENTION: Improved Method for Detection of ATP  
 W--> 95 <130> FILE REFERENCE: 10743-6  
 W--> 95 <130> FILE REFERENCE: 10743-6  
 W--> 97 <140> CURRENT APPLICATION NUMBER: US 09/813,279  
 99 <141> CURRENT FILING DATE: 2001-03-19  
 W--> 101 <150> PRIOR APPLICATION NUMBER: US 60/269,526  
 W--> 102 <151> PRIOR FILING DATE: 2001-02-16  
 W--> 104 <160> NUMBER OF SEQ ID NOS: 8  
 W--> 104 <160> NUMBER OF SEQ ID NOS: 8  
 W--> 106 <170> SOFTWARE: Microsoft Word (Rich Text Format)

This section  
already shown  
on p 1

why  
are  
these  
lines  
here?

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/813,279

DATE: 08/02/2001  
TIME: 14:49:32

Input Set : A:\sequence listing.txt  
Output Set: N:\CRF3\08022001\I813279.raw

E--> 108 <210> SEQ ID NO: 1  
 109 <211> LENGTH: 544  
 110 <212> TYPE: PRT  
 111 <213> ORGANISM: Artificial Sequence  
 W--> 112 <220> FEATURE: 78-OB10  
 W--> 112 <220> FEATURE: 78-OB10  
 113 <223> OTHER INFORMATION: Mutant luciferase derived from LucPpe2  
 115 <400> SEQUENCE: 1  
 116 Met Ala Asp Lys Asn Ile Leu Tyr Gly Pro Glu Pro Phe Tyr Pro Leu  
 117 1 5 10 15  
 118 Ala Asp Gly Thr Ala Gly Glu Gln Met Phe Asp Ala Leu Ser Arg Tyr  
 119 20 25 30  
 120 Ala Asp Ile Ser Gly Cys Ile Ala Leu Thr Asn Ala His Thr Lys Glu  
 121 35 40 45  
 122 Asn Val Leu Tyr Glu Glu Phe Leu Lys Leu Ser Cys Arg Leu Ala Glu  
 123 50 55 60  
 124 Ser Phe Lys Lys Tyr Gly Leu Lys Gln Asn Asp Thr Ile Ala Val Cys  
 125 65 70 75 80  
 126 Ser Glu Asn Gly Leu Gln Phe Phe Leu Pro Val Ile Ala Ser Leu Tyr  
 127 85 90 95  
 128 Leu Gly Ile Ile Ala Ala Pro Val Ser Asp Lys Tyr Ile Glu Arg Glu  
 129 100 105 110  
 130 Leu Ile His Ser Leu Gly Ile Val Lys Pro Arg Ile Ile Phe Cys Ser  
 131 115 120 125  
 132 Lys Asn Thr Phe Gln Lys Val Leu Asn Val Lys Ser Lys Leu Lys Ser  
 133 130 135 140  
 134 Val Glu Thr Ile Ile Leu Asp Leu Asn Glu Asp Leu Gly Gly Tyr  
 135 145 150 155 160  
 136 Gln Cys Leu Asn Asn Phe Ile Ser Gln Asn Ser Asp Ser Asn Leu Asp  
 137 165 170 175  
 138 Val Lys Lys Phe Lys Pro Tyr Ser Phe Asn Arg Asp Asp Gln Val Ala  
 139 180 185 190  
 140 Leu Val Met Phe Ser Ser Gly Thr Thr Gly Val Pro Lys Gly Val Met  
 141 195 200 205  
 142 Leu Thr His Lys Asn Ile Val Ala Arg Phe Ser Leu Ala Lys Asp Pro  
 143 210 215 220  
 144 Thr Phe Gly Asn Ala Ile Asn Pro Thr Thr Ala Ile Leu Thr Val Ile  
 145 225 230 235 240  
 146 Pro Phe His His Gly Phe Gly Met Met Thr Thr Leu Gly Tyr Phe Thr  
 147 245 250 255  
 148 Cys Gly Phe Arg Val Val Leu Met His Thr Phe Glu Glu Lys Leu Phe  
 149 260 265 270  
 150 Leu Gln Ser Leu Gln Asp Tyr Lys Val Glu Ser Thr Leu Leu Val Pro  
 151 275 280 285  
 152 Thr Leu Met Ala Phe Leu Ala Lys Ser Ala Leu Val Glu Lys Tyr Asp  
 153 290 295 300  
 154 Leu Ser His Leu Lys Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys  
 155 305 310 315 320  
 156 Glu Ile Gly Glu Met Val Lys Lys Arg Phe Lys Leu Asn Phe Val Arg

*T his  
information  
already  
shown*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/813,279

DATE: 08/02/2001  
TIME: 14:49:32

Input Set : A:\sequence listing.txt  
Output Set: N:\CRF3\08022001\I813279.raw

157	325	330	335
158	Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Val Leu Ile Thr Pro		
159	340	345	350
160	Lys Gly Asp Ala Arg Pro Gly Ser Thr Gly Lys Ile Val Pro Phe His		
161	355	360	365
162	Ala Val Lys Val Val Asp Pro Thr Thr Gly Lys Ile Leu Gly Pro Asn		
163	370	375	380
164	Glu Pro Gly Glu Leu Tyr Phe Lys Gly Ala Met Ile Met Lys Gly Tyr		
165	385	390	395
166	Tyr Asn Asn Glu Glu Ala Thr Lys Ala Ile Ile Asp Asn Asp Gly Trp		
167	405	410	415
168	Leu Arg Ser Gly Asp Ile Ala Tyr Tyr Asp Asn Asp Gly His Phe Tyr		
169	420	425	430
170	Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln Val		
171	435	440	445
172	Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val		
173	450	455	460
174	Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro		
E--> 175	465	435	440
E--> 176	Ala Pro Ala Glu Ile Glu Gly Ile Leu Leu Gln His Pro Tyr Ile Val		
E--> 177	450	455	460
E--> 178	Asp Ala Gly Val Thr Gly Ile Pro Asp Glu Ala Ala Gly Glu Leu Pro		
E--> 179	465	470	475
E--> 180	Ala Ala Gly Val Val Val Gln Thr Gly Lys Tyr Leu Asn Glu Gln Ile		
E--> 181	485	490	495
E--> 182	Val Gln Asp Tyr Val Ala Ser Gln Val Ser Thr Ala Lys Trp Leu Arg		
E--> 183	500	505	510
E--> 184	Gly Gly Val Lys Phe Leu Asp Glu Ile Pro Lys Gly Ser Thr Gly Lys		
E--> 185	515	520	525
E--> 186	Ile Asp Arg Lys Val Leu Arg Gln Met Phe Glu Lys His Thr Asn Gly		
E--> 187	530	535	540
E--> 188	<210> SEQ ID NO: 3		
454	<210> SEQ ID NO: 8		
455	<211> LENGTH: 1639		
456	<212> TYPE: DNA		
457	<213> ORGANISM: Artificial Sequence		

W--> 458 <220> FEATURE: 146-1H2 do not exist a response to 12w1  
459 <223> OTHER INFORMATION: Mutant luciferase derived from LucPpe2  
461 <400> SEQUENCE: 8

C--> 462 ggatccaatg gcagataaga atatttata tggcccgaa ccattttatc ccttggaaa 60 all bases  
463 tggacggct ggagaacaga tggatgcgc attatctcgat tatgcagacta ttccggctg 120 must be  
464 catagcatgg acaaatgctc atacaaaaga aaatgttttata tatgaagagt ttctgaaact 180 in lower-case  
465 gtcgtgtcgat ttagcgaaa gttttaaaaa gtatggatta aaacaaaacg acacaatgg 240 letters,  
466 ggtgtgtatc gaaaatagtc tgcaatttt ctttcctgtat attgcatacat tttatctgg 300  
467 aataattgtg gcacctgtta acgataaaata cattgaacgt gaattaatac acagtcttgg 360  
468 tattgtaaaa ccacccatag tttttgtctc caagaatact tttcaaaaag tactaatgt 420  
469 aaaatctaa ttaaaatcta ttgaaaactat tattatatta gacttaaaatg aagacttgg 480  
470 agtttatcaa tgcctcaaca actttatttc tcaaaattcc gatagtaatc tggacgtaaa 540

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/813,279

DATE: 08/02/2001  
TIME: 14:49:32

Input Set : A:\sequence listing.txt  
Output Set: N:\CRF3\08022001\I813279.raw

471	aaaatttaaa	ccctattctt	ttaatcgaga	cgatcagggtt	gcgtcgatttt	tgttttcttc	600
472	tggtaaca	act ggtctgccga	agggagtcat	gctaactcac	aagaatattt	ttgcacgatttt	660
473	ttcttattgca	aaagatccta	ctttggtaa	cgcaattaat	cccacgttag	caattttaac	720
474	gtaataacct	ttccaccatg	gttttggat	gatgaccaca	tttaggatact	ttacttgtgg	780
475	ttcccgagtt	gttctaatgc	acacgtttga	agaaaaacta	tttctacaat	cattacaaga	840
476	ttataaaagt	gaaagtactt	tacttgtacc	aacattaatg	gcatttcttg	caaaaagtgc	900
477	attagttgaa	aagtacgatt	tatcgcactt	aaaagaaattt	gcatctgggt	gccccaccttt	960
478	atcaaaagaa	attggggaga	tggtaaaaaa	acggttttaa	ttaaactttt	tcaggcaagg	1020
479	gtatggatta	acagaaaacca	cttcggctgt	ttaatttaca	ccgaaaagggt	acgccaaacc	1080
480	gggatcaact	ggtaaaaatag	taccattaca	cgctgttaaa	gttgcgcata	ctacaacagg	1140
481	aaaaattttg	ggccaaatg	aacctggaga	attgtatTTT	aaaggcccg	tgataatgaa	1200
482	gggttattat	aataatgaag	aagctactaa	agcaattattt	gataatgacg	gatggttgcg	1260
483	ctctggtgat	attgttattt	atgacaatga	tggccatttt	tatatttgtgg	acaggctgaa	1320
484	gtcactgatt	aaatataaag	gttatcagtt	tgcacctgct	gaaatttgggg	gaatactctt	1380
485	acaacatccg	tatattgttg	atgcggcggt	tactggtata	ccggatgaag	ccgcggggcga	1440
486	gcttccagct	gcagggttt	tagtacagac	tggaaaaat	ctaaacgaac	aaatcgata	1500
487	agattatgtt	gccagtcaag	tttcaacagc	caaatggcta	cgtgggtgggg	tggaaattttt	1560
488	ggatgaaattt	cccaaaggat	caactggaaa	aatttgcac	aaagtgttaa	gacaaatgttt	1620
489	agaaaaacac	accaatgggg					1639

E--> 494 6

*delete*

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/813,279

DATE: 08/02/2001  
TIME: 14:49:33

Input Set : A:\sequence listing.txt  
Output Set: N:\CRF3\08022001\I813279.raw

L:25 M:283 W: Missing Blank Line separator, <220> field identifier  
L:25 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:88 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1  
L:88 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:88 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
L:88 M:252 E: No. of Seq. differs, <211>LENGTH:Input:544 Found:482 SEQ:1  
L:89 M:280 W: Numeric Identifier already exists, <110> found multiple times  
L:89 M:281 W: Numeric Fields not Ordered, <110> not ordered!.  
L:93 M:280 W: Numeric Identifier already exists, <120> found multiple times  
L:93 M:281 W: Numeric Fields not Ordered, <120> not ordered!.  
L:95 M:280 W: Numeric Identifier already exists, <130> found multiple times  
L:95 M:281 W: Numeric Fields not Ordered, <130> not ordered!.  
L:97 M:280 W: Numeric Identifier already exists, <140> found multiple times  
L:97 M:281 W: Numeric Fields not Ordered, <140> not ordered!.  
L:99 M:280 W: Numeric Identifier already exists, <141> found multiple times  
L:99 M:281 W: Numeric Fields not Ordered, <141> not ordered!.  
L:101 M:281 W: Numeric Fields not Ordered, <150> not ordered!.  
L:102 M:281 W: Numeric Fields not Ordered, <151> not ordered!.  
L:104 M:280 W: Numeric Identifier already exists, <160> found multiple times  
L:104 M:281 W: Numeric Fields not Ordered, <160> not ordered!.  
L:106 M:280 W: Numeric Identifier already exists, <170> found multiple times  
L:108 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:1  
L:112 M:283 W: Missing Blank Line separator, <220> field identifier  
L:112 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
M:332 Repeated in SeqNo=1  
L:187 M:252 E: No. of Seq. differs, <211>LENGTH:Input:544 Found:576 SEQ:1  
L:189 M:214 E: (33) Seq.# missing, SEQ ID NO:2  
L:193 M:283 W: Missing Blank Line separator, <220> field identifier  
L:193 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:270 M:283 W: Missing Blank Line separator, <220> field identifier  
L:270 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:347 M:283 W: Missing Blank Line separator, <220> field identifier  
L:347 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:351 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=5  
L:384 M:283 W: Missing Blank Line separator, <220> field identifier  
L:384 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:388 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=6  
L:421 M:283 W: Missing Blank Line separator, <220> field identifier  
L:421 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:425 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=7  
L:458 M:283 W: Missing Blank Line separator, <220> field identifier  
L:458 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:462 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=8  
L:494 M:254 E: No. of Bases conflict, LENGTH:Input:6 Counted:1639 SEQ:8